

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/774,018

Source: 1FW0

Date Processed by STIC: 10/20/04

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RAW SEQUENCE LISTING

DATE: 10/20/2004

PATENT APPLICATION: US/10/774,018

TIME: 16:28:37

Input Set : A:\HENK0060.ST25.txt

Output Set: N:\CRF4\10202004\J774018.raw

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3 <110> APPLICANT: Kottwitz, Beatrix
4     Breves, Roland
5     Maurer, Karl-Heinz
7 <120> TITLE OF INVENTION: DETERGENT AND CLEANING AGENT WITH HYBRID ALPHA-AMYLASES
9 <130> FILE REFERENCE: HENK-0060 / H4714
11 <140> CURRENT APPLICATION NUMBER: US 10/774,018
12 <141> CURRENT FILING DATE: 2004-02-06
14 <150> PRIOR APPLICATION NUMBER: PCT/EP02/08391
15 <151> PRIOR FILING DATE: 2002-07-27
17 <150> PRIOR APPLICATION NUMBER: EP 101 38 753.9
18 <151> PRIOR FILING DATE: 2001-08-07
20 <160> NUMBER OF SEQ ID NOS: 20
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1452
26 <212> TYPE: DNA
27 <213> ORGANISM: Bacillus licheniformis
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1449)
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37 1          5          10          15
39 aat gac ggc caa cat tgg aag cgc ttg caa aac gac tcg gca tat ttg      96
40 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
41 20          25          30
43 gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga      144
44 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
45 35          40          45
47 acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta      192
48 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
49 50          55          60
51 ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa      240
52 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
53 65          70          75          80
55 gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac      288
56 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
57 85          90          95
59 gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc      336
60 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
61 100         105         110
63 gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta      384

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64	Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	
65			115						120				125				
67	att	tca	gga	gaa	cac	cga	att	aaa	gcc	tgg	aca	cat	ttt	cat	ttt	ccg	432
68	Ile	Ser	Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	
69		130						135					140				
71	ggg	cgc	ggc	agc	aca	tac	agc	gat	ttt	aaa	tgg	cat	tgg	tac	cat	ttt	480
72	Gly	Arg	Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	
73	145						150				155				160		
75	gac	gga	acc	gat	tgg	gac	gag	tcc	cga	aag	ctg	aac	cgc	atc	tat	aag	528
76	Asp	Gly	Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	
77			165						170				175				
79	ttt	caa	gga	aag	gct	tgg	gat	tgg	gaa	gtt	tcc	aat	gaa	aac	ggc	aac	576
80	Phe	Gln	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	
81			180						185				190				
83	tat	gat	tat	ttg	atg	tat	gcc	gac	atc	gat	tat	gac	cat	cct	gat	gtc	624
84	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	
85		195						200					205				
87	gca	gca	gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	672
88	Ala	Ala	Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	
89		210						215				220					
91	ttg	gac	ggt	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	720
92	Leu	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	
93	225				230					235				240			
95	ttg	cgg	gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	768
96	Leu	Arg	Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	
97			245						250				255				
99	ttt	acg	gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	816
100	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	
101			260						265				270				
103	tat	ttg	aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	864
104	Tyr	Leu	Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	
105			275					280					285				
107	cat	tat	cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	912
108	His	Tyr	Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	
109		290					295				300						
111	agg	aaa	ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	960
112	Arg	Lys	Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	
113	305				310					315				320			
115	gtt	aca	ttt	gtc	gat	aac	cat	gat	aca	cag	ccg	ggg	caa	tcg	ctt	gag	1008
116	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	
117			325						330				335				
119	tcg	act	gtc	caa	aca	tgg	ttt	aag	ccg	ctt	gct	tac	gct	ttt	att	ctc	1056
120	Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	
121			340						345				350				
123	aca	agg	gaa	tct	gga	tac	cct	cag	gtt	ttc	tac	ggg	gat	atg	tac	ggg	1104
124	Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	
125			355					360					365				
127	acg	aaa	gga	gac	tcc	cag	cgc	gaa	att	cct	gcc	ttg	aaa	cac	aaa	att	1152
128	Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	

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129      370      375      380
131 gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat      1200
132 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
133 385      390      395      400
135 gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac      1248
136 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
137      405      410      415
139 agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc      1296
140 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
141      420      425      430
143 ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca      1344
144 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
145      435      440      445
147 tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg      1392
148 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
149      450      455      460
151 gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat      1440
152 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
153 465      470      475      480
155 gtt caa aga tag      1452
156 Val Gln Arg
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 483
162 <212> TYPE: PRT
163 <213> ORGANISM: Bacillus licheniformis
165 <400> SEQUENCE: 2
167 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
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171 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
172      20      25      30
175 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
176      35      40      45
179 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
180      50      55      60
183 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
184 65      70      75      80
187 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
188      85      90      95
191 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
192      100      105      110
195 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
196      115      120      125
199 Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro
200      130      135      140
203 Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
204 145      150      155      160
207 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
208      165      170      175
211 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn

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212          180          185          190
215 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
216          195          200          205
219 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
220          210          215          220
223 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
224 225          230          235          240
227 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
228          245          250          255
231 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
232          260          265          270
235 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
236          275          280          285
239 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
240          290          295          300
243 Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
244 305          310          315          320
247 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
248          325          330          335
251 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
252          340          345          350
255 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
256          355          360          365
259 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
260          370          375          380
263 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
264 385          390          395          400
267 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
268          405          410          415
271 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
272          420          425          430
275 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
276          435          440          445
279 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
280          450          455          460
283 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
284 465          470          475          480
287 Val Gln Arg
291 <210> SEQ ID NO: 3
292 <211> LENGTH: 1452
293 <212> TYPE: DNA
294 <213> ORGANISM: Bacillus amyloliquefaciens
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (1)..(1449)
301 <400> SEQUENCE: 3
302 gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac
303 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
304 1          5          10          15

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48

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306	ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
307	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
308				20					25					30			
310	atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga	ttg	agc	144
311	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser	
312			35					40					45				
314	caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	gga	gaa	192
315	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
316		50					55				60						
318	ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	tca	gag	240
319	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu	
320	65					70				75					80		
322	ctt	caa	gat	gcg	atc	ggc	tca	ctg	cat	tcc	cgg	aac	gtc	caa	gta	tac	288
323	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	
324				85					90				95				
326	gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggt	gct	gat	gca	aca	gaa	gat	336
327	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
328			100					105				110					
330	gta	act	gcc	gtc	gaa	gtc	aat	ccg	gcc	aat	aga	aat	cag	gaa	act	tcg	384
331	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	
332			115				120					125					
334	gag	gaa	tat	caa	atc	aaa	gcg	tgg	acg	gat	ttt	cgt	ttt	ccg	ggc	cgt	432
335	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg	
336		130				135				140							
338	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	gac	gga	480
339	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
340	145				150				155				160				
342	gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	ttt	cgt	528
343	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg	
344			165					170				175					
346	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	ggc	aac	576
347	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn	
348			180				185				190						
350	tat	gac	tat	tta	atg	tat	gct	gat	gtt	gac	tac	gac	cac	cct	gat	gtc	624
351	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val	
352		195				200				205							
354	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	ctg	tca	672
355	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	
356		210				215				220							
358	tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	720
359	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	
360	225				230				235				240				
362	ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	gaa	atg	768
363	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	
364			245				250				255						
366	ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	816
367	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	
368			260				265				270						
370	tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	ccg	ctt	864

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Valid <213> Response:

of "Artificial" only as "<213> Organism" response is incomplete,
r 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

#:5,6,7,8,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY

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